RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/857,518_

Source: _PCT/09_

Date Processed by STIC: _5/15/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

PCT09

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

Does Not Comply
Corrected Diskette Needed
*pp 1-2,4-7, 9-11,
13-16, 18-24*

```
   3  <110> APPLICANT: Aharoni, Asaph
   4        Lucker, Joost
   5        Verhoeven, Harrie A.
   6        van Tunen, Arjen J.
   7        O'Connell, Ann P.
   9  <120> TITLE OF INVENTION: Fruit Flavour Related Genes And Use Thereof
  11  <130> FILE REFERENCE: 160721
  13  <140> CURRENT APPLICATION NUMBER: US/09/857,518
  14  <141> CURRENT FILING DATE: 2002-03-29
  16  <150> PRIOR APPLICATION NUMBER: EP 98204018.0
  17  <151> PRIOR FILING DATE: 1998-12-02
  19  <150> PRIOR APPLICATION NUMBER: EP 99200739.3
  20  <151> PRIOR FILING DATE: 1999-03-12
  22  <160> NUMBER OF SEQ ID NOS: 50
  24  <170> SOFTWARE: PatentIn Ver. 2.1
```

ERRORED SEQUENCES

```
 763  <210> SEQ ID NO: 6
 764  <211> LENGTH: 452
 765  <212> TYPE: PRT
 768  <213> ORGANISM: Fragaria x ananassa          → <220>  ← insert this mandatory
 769  <223> OTHER INFORMATION: Strawberry alcohol acyl transferase       numeric identifier
 771  <400> SEQUENCE: 6                                             whenever <221>
 772  Met Glu Lys Ile Glu Val Ser Ile Asn Ser Lys His Thr Ile Lys Pro   <222>, or <223>
 773   1               5                  10                  15
 775  Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp   is shown
 776              20                  25                  30
 778  Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe Phe Tyr Pro Ile   (global error)
 779          35                  40                  45
 781  Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala Asp Leu Arg Gln
 782      50                  55                  60
 784  Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
 785  65                  70                  75                  80
 787  Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
 788                  85                  90                  95
 790  Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys
 791              100                 105                 110
 793  Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
 794          115                 120                 125
 796  Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val
 797      130                 135                 140
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

```
799 Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
800 145               150               155                   160
802 Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe
803               165               170                   175
805 Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala
806               180               185                   190
808 Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln
809           195               200               205
813 Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala Thr Arg Arg Phe
814       210               215               220
816 Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser
817 225               230               235                   240
819 Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu
820               245               250               255
822 Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr
823           260               265               270
825 Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg
826           275               280               285
828 Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp
829       290               295               300
831 Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser
832 305               310               315                   320
834 Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
835           325               330               335
837 Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
838           340               345               350
840 Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
841           355               360               365
843 Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
844       370               375               380
846 Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
847 385               390               395                   400
849 Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
850               405               410                   415
852 Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
853           420               425               430
855 Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro
858           435               440               445
860 Lys Thr Leu Ile
861       450
1680 <210> SEQ ID NO: 14
1681 <211> LENGTH: 434
1682 <212> TYPE: PRT
1683 <213> ORGANISM: Citrus limon                    <2207Insert
1684 <223> OTHER INFORMATION: Citrus limon alcohol acyl transferase
1686 <400> SEQUENCE: 14
1687 Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln Glu
1688   1               5               10                  15
1690 Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val Pro
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

```
1691                  20                      25                      30
1693 Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp Cys
1694         35                      40                      45
1696 Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu Val
1697     50                      55                      60
1699 Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu Asn
1700 65                      70                      75                      80
1702 Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu Glu
1703                 85                      90                      95
1705 Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln Gly
1706             100                     105                     110
1708 Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp Ile
1709             115                     120                     125
1713 Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys Gly
1714         130                     135                     140
1716 Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly Ala
1717 145                     150                     155                     160
1719 Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly Val
1720             165                     170                     175
1722 Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val Gly
1723             180                     185                     190
1725 Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro Pro
1726             195                     200                     205
1728 Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr Ala
1729         210                     215                     220
1731 Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys Ser
1732 225                     230                     235                     240
1734 Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile Leu
1735             245                     250                     255
1737 Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser Asp
1738             260                     265                     270
1740 Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg Leu
1741         275                     280                     285
1743 Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Thr
1744         290                     295                     300
1746 Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn His
1747 305                     310                     315                     320
1749 Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu Tyr
1750             325                     330                     335
1752 Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn Ala
1753             340                     345                     350
1755 Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile Val
1758             355                     360                     365
1760 Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly Gln
1761         370                     375                     380
1763 Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala His
1764 385                     390                     395                     400
1766 Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile Asn
1767             405                     410                     415
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

1769 Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu Ile
1770   420   425   430
1772 Phe Asp
2324 <210> SEQ ID NO: 19
2325 <211> LENGTH: 455
2326 <212> TYPE: PRT
2327 <213> ORGANISM: Fragaria vesca   → <220> insert
2328 <223> OTHER INFORMATION: Strawberry vesca alcohol acyl transferase
2330 <400> SEQUENCE: 19
2331 Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro
2332 1   5   10   15
2334 Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
2335   20   25   30
2337 Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
2338   35   40   45
2340 Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His
2343   50   55   60
2345 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
2346 65   70   75   80
2348 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
2349   85   90   95
2351 Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys
2352   100   105   110
2354 Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
2355   115   120   125
2357 Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile
2358   130   135   140
2360 Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
2361 145   150   155   160
2363 Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe
2364   165   170   175
2366 Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala
2367   180   185   190
2369 Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln
2370   195   200   205
2372 Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe
2373   210   215   220
2375 Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser
2376 225   230   235   240
2378 Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu
2379   245   250   255
2381 Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
2382   260   265   270
2384 Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
2385   275   280   285
2388 Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp
2389   290   295   300
2391 Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser
2392 305   310   315   320

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

```
2394 Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
2395             325             330             335
2397 Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr
2398         340             345             350
2400 Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
2401         355             360             .       365
2403 Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe
2404     370             375             380
2406 Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
2407 385             390             395             400
2409 Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
2410             405             410             415
2412 Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
2413         420             425             430.
2415 Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
2416         435             440     .       445
2418 Lys Thr Leu Ile Ser Arg Tyr
2419     450             455
2421 <210> SEQ ID NO: 20
2422 <211> LENGTH: 419
2423 <212> TYPE: PRT
2424 <213> ORGANISM: Musa sp
2425 <223> OTHER INFORMATION: Banana alcohol acyl transferase
2427 <400> SEQUENCE: 20
2428 Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
2429  1               5               10              15
2433 Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
2434             20              25              30
2436 Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
2437         35              40              45
2439 Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
2440     50              55              60
2442 Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
2443 65              70              75              80
2445 Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
2446             85              90      .       95
2448 Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
2449             100             105             110
2451 Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
2452         115             120             125
2454 Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
2455     130             135             140
2457 Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
2458 145             150     .       155             160
2460 Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
2461             165             170             175
2463 Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
2464             180             185             190
2466 Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
```

```
2467           195                    200                    205
2469 Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
2470      210                    215                    220
2472 Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
2473 225                    230                    235                    240
2475 Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn
2478                    245                    250                    255
2480 Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
2481           260                    265                    270
2483 His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
2484           275                    280                    285
2486 Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
2487           290                    295                    300
2489 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
2490 305                    310                    315                    320
2492 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
2493           325                    330                    335
2495 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
2496           340                    345                    350
2498 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
2499           355                    360                    365
2501 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
2502      370                    375                    380
2504 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
2505 385                   ·390                    395                    400
2507 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
2508                    405                    410                    415
2510 Gly Phe Ala
2512 <210> SEQ ID NO: 21
2513 <211> LENGTH: 454
2514 <212> TYPE: PRT
2515 <213> ORGANISM: Malus sp.
2516 <223> OTHER INFORMATION: Apple alcohol acyl transferase
2518 <400> SEQUENCE: 21
2519 Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile
2520   1                5                   10                   15
2523 Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
2524           20                   25                   30
2526 Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr
2527           35                   40                   45
2529 Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile
2530      50                   55                   60
2532 Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
2533 65                   70                   75                   80
2535 Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
2536           85                   90                   95
2538 Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
2539           100                   105                   110
2541 Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu
```

Handwritten annotations: "<2207 insert" near line 2515; marginal mark near line 2518.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,518

DATE: 05/15/2002
TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

```
2542          115                  120                  125
2544 Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu
2545       130                  135                  140
2547 Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg
2548 145                  150                  155                  160
2550 Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr
2551                  165                  170                  175
2553 Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro
2554                  180                  185                  190
2556 Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr
2557                  195                  200                  205
2559 Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser
2560       210                  215                  220
2562 Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe
2563 225                  230                  235                  240
2565 Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu
2568                  245                  250                  255
2570 Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys
2571                  260                  265                  270
2573 Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val
2574                  275                  280                  285
2576 Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro
2577       290                  295                  300
2579 Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys
2580 305                  310                  315                  320
2582 Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val
2583                  325                  330                  335
2585 Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala
2586                  340                  345                  350
2588 Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser
2589                  355                  360                  365
2591 Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn
2592       370                  375                  380
2594 Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp
2595 385                  390                  395                  400
2597 Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile
2598                  405                  410                  415
2600 Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln
2601                  420                  425                  430
2603 Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn
2604                  435                  440                  445
2606 Leu Arg Ser Thr Ser Gln
2607       450
2609 <210> SEQ ID NO: 22
2610 <211> LENGTH: 431
2613 <212> TYPE: PRT
2614 <213> ORGANISM: Mangifera indica        ⟶⟨2207⟩ insert
2615 <223> OTHER INFORMATION: Mango alcohol acyl transferase
2617 <400> SEQUENCE: 22
```

```
2618 Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu
2619  1              5                   10                  15
2621 Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro
2622          20                  25                  30
2624 Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile
2625          35                  40                  45
2627 Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu
2628          50                  55                  60
2630 Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly
2631  65                  70                  75                  80
2633 Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala
2634          85                  90                  95
2636 Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu
2637          100                 105                 110
2639 Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser
2640          115                 120                 125
2642 Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly
2643          130                 135                 140
2645 Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser
2646 145                 150                 155                 160
2648 Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
2649          165                 170                 175
2651 Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp
2652          180                 185                 190
2654 Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro
2655          195                 200                 205
2658 Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
2659          210                 215                 220
2661 Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
2662 225                 230                 235                 240
2664 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
2665          245                 250                 255
2667 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
2668          260                 265                 270
2670 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
2671          275                 280                 285
2673 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
2674          290                 295                 300
2676 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
2677 305                 310                 315                 320
2679 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
2680          325                 330                 335
2682 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
2683          340                 345                 350
2685 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
2686          355                 360                 365
2688 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
2689          370                 375                 380
2691 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
```

```
2692 385                    390                395                400
2694 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
2695                    405                410                415
2697 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
2698                420                425                430
2700 <210> SEQ ID NO: 23
2703 <211> LENGTH: 426
2704 <212> TYPE: PRT
2705 <213> ORGANISM: Citrus limon                →<220> insert
2706 <223> OTHER INFORMATION: Lemon acyl transferase
2708 <400> SEQUENCE: 23
2709 Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro
2710  1              5                10                15
2712 Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu
2713            20                25                30
2715 Thr Pro Asn Val Tyr Phe Ser Ile Ile Leu Leu Tyr Ser Lys Ala Gly
2716            35                40                45
2718 Glu Ser Thr Ala Lys Thr Ser Asp His Leu Lys Glu Ser Leu Ser Asn
2719        50                55                60
2721 Thr Leu Thr His Tyr Tyr Pro Leu Ala Gly Gln Leu Lys Tyr Asp Gln
2722 65                70                75                80
2724 Leu Ile Val Asp Cys Asn Asp Gln Gly Val Pro Phe Ile Glu Ala His
2725                85                90                95
2727 Val Thr Asn Asp Met Arg Gln Leu Leu Lys Ile Pro Asn Ile Asp Val
2728            100                105                110
2730 Leu Glu Gln Leu Leu Pro Phe Lys Pro His Glu Gly Phe Asp Ser Asp
2731            115                120                125
2733 Arg Ser Asn Leu Thr Val Gln Val Asn Tyr Phe Gly Cys Glu Gly Met
2734        130                135                140
2736 Ala Ile Gly Leu Cys Phe Arg His Lys Val Ile Asp Ala Thr Thr Ala
2737 145                150                155                160
2739 Ala Phe Phe Val Lys Asn Trp Gly Val Ile Ala Arg Gly Ala Gly Glu
2740            165                170                175
2742 Ile Lys Asp Val Ile Ile Asp His Ala Ser Leu Phe Pro Ala Arg Asp
2743            180                185                190
2745 Leu Ser Cys Leu Thr Lys Ser Val Asp Glu Glu Phe Leu Lys Pro Glu
2748            195                200                205
2750 Ser Glu Thr Lys Arg Phe Val Phe Asp Gly Ala Thr Ile Ala Ser Leu
2751        210                215                220
2753 Gln Glu Thr Phe Ala Ser Phe Glu Arg Arg Pro Thr Arg Phe Glu Val
2754 225                230                235                240
2756 Val Ser Ala Val Ile Leu Gly Ala Leu Ile Thr Ala Thr Arg Glu Ser
2757            245                250                255
2759 Asp Asp Glu Ser Asn Val Pro Glu Arg Leu Asp Thr Ile Ile Ser Val
2760            260                265                270
2762 Asn Leu Arg Gln Arg Met Asn Pro Pro Phe Pro Glu His Cys Met Gly
2763        275                280                285
2765 Asn Ile Ile Ser Gly Gly Leu Val Tyr Trp Pro Leu Glu Lys Lys Val
2766        290                295                300
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

2768 Asp Tyr Gly Cys Leu Ala Lys Glu Ile His Glu Ser Ile Lys Lys Val
2769 305   310   315   320
2771 Asp Asp Gln Phe Ala Arg Lys Phe Tyr Gly Asp Ala Glu Phe Leu Asn
2772   325   330   335
2774 Leu Pro Arg Leu Ala Gly Ala Glu Asp Val Lys Lys Arg Glu Phe Trp
2775   340   345   350
2777 Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp
2778   355   360   365
2780 Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr
2781   370   375   380
2783 Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly
2784 385   390   395   400
2786 Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu
2787   405   410   415
2789 Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe
2790   420   425
2793 <210> SEQ ID NO: 24
2794 <211> LENGTH: 491
2795 <212> TYPE: PRT
2796 <213> ORGANISM: Citrus limon   3(2267
2797 <223> OTHER INFORMATION: Lemon acyl transferase
2799 <400> SEQUENCE: 24
2800 Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr
2801   1   5   10   15
2803 Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr
2804   20   25   30
2806 Leu Asp Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val
2807   35   40   45
2809 Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe
2810   50   55   60
2812 Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu
2813 65   70   75   80
2815 Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala
2816   85   90   95
2818 Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser
2819   100   105   110
2821 Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His
2822   115   120   125
2824 Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val
2825   130   135   140
2827 Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln
2828 145   150   155   160
2830 Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His
2831   165   170   175
2833 His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp
2834   180   185   190
2838 Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser
2839   195   200   205
2841 Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr

```
2842      210                    215                  220
2844 Gly Gln Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn
2845 225                  230                  235                 240
2847 Ser Asp Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp
2848                  245                  250                  255
2850 Ser Glu Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg
2851              260                  265                  270
2853 Glu Asp Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys
2854          275                  280                  285
2856 Ser Ser Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu
2857          290                  295                  300
2859 Ala Tyr Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys
2860 305                  310                  315                 320
2862 Thr Glu Ala Glu Ala Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile
2863                  325                  330                  335
2865 Val Gly Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro
2866              340                  345                  350
2868 Leu Asn Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys
2869          355                  360                  365
2871 Ala Ser Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met
2872          370                  375                  380
2874 Leu Ser Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn
2875 385                  390                  395                 400
2877 Asp Asp Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met
2878              405                  410                  415
2880 Ile Phe Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp
2883              420                  425                  430
2885 Phe Gly Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg
2886          435                  440                  445
2888 Thr Gln Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Gly Val
2889      450                  455                  460
2891 Glu Val Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser
2892 465                  470                  475                 480
2894 Val Phe Ala Asp Gly Leu Lys Asn Asp Leu Val
2895              485                  490
2897 <210> SEQ ID NO: 25
2898 <211> LENGTH: 447
2899 <212> TYPE: PRT
2900 <213> ORGANISM: Citrus limon                9(2207
2901 <223> OTHER INFORMATION: Lemon acyl transferase
2903 <400> SEQUENCE: 25
2904 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro
2905 1                5                  10                  15
2907 Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp Ser
2908              20                  25                  30
2910 Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg Pro
2911          35                  40                  45
2913 Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser Ala
2914      50                  55                  60
```

```
2916 Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val Arg
2917  65                  70                  75                  80
2919 Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly Gln
2920                  85                  90                  95
2922 Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr Asp
2923             100                 105                 110
2925 Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu Ser
2928             115                 120                 125
2930 Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val Gln
2931     130                 135                 140
2933 Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn
2934 145                 150                 155                 160
2936 His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe
2937             165                 170                 175
2939 Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His Ser
2940             180                 185                 190
2942 Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser Ser
2943             195                 200                 205
2945 Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu
2946     210                 215                 220
2948 Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser Asn
2949 225                 230                 235                 240
2951 Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn
2952             245                 250                 255
2954 Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu Ala
2955             260                 265                 270
2957 Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala
2958             275                 280                 285
2960 Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe Ser
2961     290                 295                 300
2963 Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr
2964 305                 310                 315                 320
2966 Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu
2967             325                 330                 335
2969 Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys
2970             340                 345                 350
2973 Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser
2974             355                 360                 365
2976 His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln
2977     370                 375                 380
2979 Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro
2980 385                 390                 395                 400
2982 Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro
2983             405                 410                 415
2985 Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr
2986             420                 425                 430
2988 Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
2989             435                 440                 445
2991 <210> SEQ ID NO: 26
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

2992 <211> LENGTH: 456
2993 <212> TYPE: PRT
2994 <213> ORGANISM: Cucumis melo   )(2207 insert
2995 <223> OTHER INFORMATION: Honey dew melon alcohol acyl transferase
2997 <400> SEQUENCE: 26
2998 Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
2999 1   5   10   15
3001 Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
3002   20   25   30
3004 Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
3005   35   40   45
3007 His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
3008   50   55   60
3010 Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
3011 65   70   75   80
3013 Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
3014   85   90   95
3018 Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
3019   100   105   110
3021 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
3022   115   120   125
3024 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile
3025   130   135   140
3027 Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe
3028 145   150   155   160
3030 Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala
3031   165   170   175
3033 Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val
3034   180   185   190
3036 Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe
3037   195   200   205
3039 Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile
3040   210   215   220
3042 Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln
3043 225   230   235   240
3045 Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro
3046   245   250   255
3048 Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala
3049   260   265   270
3051 Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn
3052   275   280   285
3054 Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val
3055   290   295   300
3057 Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro
3058 305   310   315   320
3060 Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr
3063   325   330   335
3065 Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg
3066   340   345   350

```
3068 Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg
3069         355             360             365
3071 Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly
3072         370             375             380
3074 Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe
3075 385             390             395             400
3077 Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser
3078             405             410             415
3080 Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His
3081         420             425             430
3083 Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met
3084         435             440             445
3086 Gln Thr Ile Gln Ser Ala Ser Lys
3087     450             455
3089 <210> SEQ ID NO: 27
3090 <211> LENGTH: 397
3091 <212> TYPE: PRT
3092 <213> ORGANISM: Fragaria x ananassa
3093 <223> OTHER INFORMATION: Strawberry aminotransferase
3095 <400> SEQUENCE: 27
3096 Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro Glu Ile Ala Arg Arg
3097  1               5               10              15
3099 Arg Asn Ala His Leu Gln Lys His Pro Asp Ala Lys Ile Ile Pro Leu
3100             20              25              30
3102 Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala
3103             35              40              45
3105 Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly
3108         50              55              60
3110 Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys
3111  65              70              75              80
3113 Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser
3114             85              90              95
3116 Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala
3117             100             105             110
3119 Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp
3120         115             120             125
3122 Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln
3123     130             135             140
3125 Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe
3126 145             150             155             160
3128 Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys
3129             165             170             175
3131 Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr
3132             180             185             190
3134 Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp
3135         195             200             205
3137 Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe
3138     210             215             220
3140 Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser
```

```
3141 225                 230                 235                 240
3143 Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro
3144                 245                 250                 255
3146 Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn
3147                 260                 265                 270
3149 Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala
3150             275                 280                 285
3153 Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly
3154         290                 295                 300
3156 Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe
3157 305                 310                 315                 320
3159 Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val
3160                 325                 330                 335
3162 Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile
3163             340                 345                 350
3165 Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro
3166         355                 360                 365
3168 Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn
3169         370                 375                 380
3171 Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys
3172 385                 390                 395
3174 <210> SEQ ID NO: 28
3175 <211> LENGTH: 458
3176 <212> TYPE: PRT
3177 <213> ORGANISM: Fragaria x ananassa              →(2267
3178 <223> OTHER INFORMATION: Strawberry thiolase
3180 <400> SEQUENCE: 28
3181 Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg
3182   1                 5                 10                  15
3184 Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala
3185                 20                 25                  30
3187 Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp
3188             35                 40                  45
3190 Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg
3191         50                 55                  60
3193 Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu
3194  65                 70                 75                  80
3198 Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp
3199                 85                 90                  95
3201 Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu
3202             100                 105                 110
3204 Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val
3205         115                 120                 125
3207 Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp
3208         130                 135                 140
3210 Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala
3211 145                 150                 155                 160
3213 Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val
3214             165                 170                 175
```

```
3216 Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro
3217         180             185             190
3219 Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg
3220         195             200             205
3222 Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala
3223     210             215             220
3225 Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr
3226 225             230             235             240
3228 Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser
3229             245             250             255
3231 Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu
3232             260             265             270
3234 Lys Pro Val Phe Lys Lys Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser
3235         275             280             285
3237 Gln Val Ser Asp Gly Ala Gly Ala Val Leu Leu Met Lys Arg Ser Val
3238     290             295             300
3240 Ala Asp Gln Lys Gly Leu Pro Ile Leu Gly Val Phe Arg Asn Phe Val
3243 305             310             315             320
3245 Ala Val Gly Val Asp Pro Ala Ile Met Gly Val Gly Pro Ala Ala Ala
3246             325             330             335
3248 Ile Pro Val Ala Val Lys Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp
3249             340             345             350
3251 Leu Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg
3252         355             360             365
3254 Asn Lys Leu Gly Leu Asp Pro Glu Lys Ile Asn Val Asn Gly Gly Ala
3255     370             375             380
3257 Met Ala Ile Gly His Pro Leu Gly Ala Thr Gly Ala Arg Cys Val Ala
3258 385             390             395             400
3260 Thr Leu Leu His Glu Met Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly
3261             405             410             415
3263 Val Ile Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala Ala Val Phe
3264             420             425             430
3266 Glu Arg Gly Asp Arg Thr Asp Glu Leu Cys Asn Ala Arg Lys Val Glu
3267         435             440             445
3269 Ser Leu Asn Phe Leu Ser Lys Asp Val Arg
3270     450             455
3272 <210> SEQ ID NO: 29
3273 <211> LENGTH: 605
3274 <212> TYPE: PRT
3275 <213> ORGANISM: Fragaria x ananassa      ⟶ ⟨2207 insert
3276 <223> OTHER INFORMATION: Strawberry pyruvate decarboxylase
3278 <400> SEQUENCE: 29
3279 Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His
3280 1           5               10              15
3282 Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser
3283             20              25              30
3285 Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His
3288         35              40              45
3290 Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val
```

```
3291      50              ·      55                     60
3293 Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro
3294  65                 70                 75                     80
3296 Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala
3297                     85                 90                 95
3299 Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr
3300                100                105                110
3302 Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr
3303                115                120                125
3305 Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn
3306        130                135                140
3308 Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp
3309 145                150                155                160
3311 Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala
3312                165                170                175
3314 Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile
3315                180                185        ·        190
3317 Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys
3318                195                200                205
3320 Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro
3321        210                215                220
3323 Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala
3324 225                230                235                240
3326 Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met
3327                245                250                255
3329 Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val
3330                260                265                270
3333 Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala
3334        275                280                285
3336 Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp
3337        290                295                300
3339 Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp
3340 305                310                315                320
3342 Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly
3343                325                330                335
3345 Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp
3346        340                345                350
3348 Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys
3349        355                360                365
3351 Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala
3352        370                375                380
3354 His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys
3355 385                390                395                400
3357 Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile
3358.                405                410                415
3360 Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp
3361        420                425                430
3363 Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr
3364        435                440                445
```

```
3366 Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr
3367       450               455               460
3369 Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile
3370 465               470               475               480
3372 Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile
3373               485               490               495
3375 Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr
3378               500               505               510
3380 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn
3381       515               520               525
3383 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys
3384       530               535               540
3386 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile
3387 545               550               555               560
3389 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val
3390               565               570               575
3392 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser
3393               580               585               590
3395 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln
3396       595               600               605
3403 <210> SEQ ID NO: 30
3404 <211> LENGTH: 333
3405 <212> TYPE: PRT
3406 <213> ORGANISM: Fragaria x ananassa
3407 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
3409 <400> SEQUENCE: 30
3410 Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp
3411 1               5               10               15
3413 Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg
3414               20               25               30
3416 Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly
3417       35               40               45
3419 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser
3420       50               55               60
3423 Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu
3424 65               70               75               80
3426 Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val
3427               85               90               95
3429 Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His
3430               100               105               110
3432 Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr
3433       115               120               125
3435 Tyr Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala
3436       130               135               140
3438 Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly
3439 145               150               155               160
3441 Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg
3442               165               170               175
3444 Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu
```

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

```
3445           180              185                190
3447 Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val
3448           195              200              205
3450 Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg
3451      210              215              220
3453 Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln
3454 225              230              235                240
3456 Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser
3457           245              250                255
3459 Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly
3460           260              265              270
3462 Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val
3463           275              280              285
3465 Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly
3468      290              295              300
3470 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn
3471 305              310              315                320
3473 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
3474           325              330
3476 <210> SEQ ID NO: 31
3477 <211> LENGTH: 326
3478 <212> TYPE: PRT
3479 <213> ORGANISM: Fragaria x ananassa
3480 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
3482 <400> SEQUENCE: 31
3483 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
3484   1              5                10                15
3486 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
3487           20              25              30
3489 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
3490           35              40              45
3492 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
3493      50              55              60
3495 Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
3496 65              70              75                80
3498 Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
3499           85              90              95
3501 Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp
3502           100              105              110
3504 Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
3505           115              120              125
3507 Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr
3508      130              135              140
3510 Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg
3513 145              150              155                160
3515 Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser
3516           165              170              175
3518 Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr
3519           180              185              190
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

          Input Set : A:\EP.txt
          Output Set: N:\CRF3\05152002\I857518.raw

```
3521 Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp
3522         195             200             205
3524 Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val
3525         210             215             220
3527 Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn
3528 225             230             235             240
3530 Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro
3531         245             250             255
3533 Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile
3534         260             265             270
3536 Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His
3537         275             280             285
3539 Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr
3540         290             295             300
3542 Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile
3543 305             310             315             320
3545 Asp Val Glu Asn Thr Leu
3546             325
3548 <210> SEQ ID NO: 32
3549 <211> LENGTH: 278
3550 <212> TYPE: PRT
3551 <213> ORGANISM: Fragaria x ananassa
3552 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
3554 <400> SEQUENCE: 32
3555 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu
3558  1               5               10              15
3560 Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn
3561         20              25              30
3563 Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly
3564         35              40              45
3566 Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala
3567         50              55              60
3569 Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro
3570 65              70              75              80
3572 Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly
3573         85              90              95
3575 Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu
3576         100             105             110
3578 Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr
3579         115             120             125
3581 Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu
3582         130             135             140
3584 Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala
3585 145             150             155             160
3587 Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His
3588             165             170             175
3590 Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val
3591         180             185             190
3593 Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser Leu
```

```
                   Input Set : A:\EP.txt
                   Output Set: N:\CRF3\05152002\I857518.raw

3594          195                 200                 205
3596 Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys
3597      210                 215                 220
3599 Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala
3600 225                 230                 235                 240
3603 Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg
3604                 245                 250                 255
3606 Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn
3607          260                 265                 270
3609 Thr Leu Lys Pro Ala Ile
3610          275
3612 <210> SEQ ID NO: 33
3613 <211> LENGTH: 283
3614 <212> TYPE: PRT
3615 <213> ORGANISM: Fragaria x ananassa
3616 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
3618 <400> SEQUENCE: 33
3619 Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg
3620   1               5                 10                  15
3622 Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile
3623              20                 25                  30
3625 Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
3626           35                 40                  45
3628 Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
3629      50                 55                 60
3631 Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
3632  65                 70                 75                 80
3634 Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
3635              85                 90                 95
3637 Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
3638          100                 105                 110
3640 Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
3641          115                 120                 125
3643 Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
3644          130                 135                 140
3648 Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr
3649 145                 150                 155                 160
3651 Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
3652              165                 170                 175
3654 Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
3655              180                 185                 190
3657 Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys
3658          195                 200                 205
3660 His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met
3661          210                 215                 220
3663 Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
3664 225                 230                 235                 240
3666 Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
3667              245                 250                 255
```

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : A:\EP.txt
Output Set: N:\CRF3\05152002\I857518.raw

```
3669 Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
3670             260                 265                 270
3672 Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
3673         275                 280
3675 <210> SEQ ID NO: 34
3676 <211> LENGTH: 188
3677 <212> TYPE: PRT
3678 <213> ORGANISM: Fragaria x ananassa      <2207 insert
3679 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
3681 <400> SEQUENCE: 34
3682 Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val
3683   1             5                 10                  15
3685 Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala
3686             20                  25                  30
3688 Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp
3689         35                  40                  45
3693 Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp
3694         50                  55                  60
3696 Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp
3697   65                  70                  75                  80
3699 Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys
3700             85                  90                  95
3702 Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu
3703             100                 105                 110
3705 Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser
3706         115                 120                 125
3708 Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala
3709         130                 135                 140
3711 Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
3712 145                 150                 155                 160
3714 Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe
3715             165                 170                 175
3717 Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
3718             180                 185
4108 <210> SEQ ID NO: 39
4109 <211> LENGTH: 181
4110 <212> TYPE: PRT
4111 <213> ORGANISM: Fragaria x ananassa   <2207 insert
4112 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
4114 <400> SEQUENCE: 39
4115 Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly
4116   1             5                 10                  15
4118 Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His
4119             20                  25                  30
4121 Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu
4122             35                  40                  45
4124 His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met
4125         50                  55                  60
4127 Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val
```

```
4128 65                    70                   75                    80
4130 Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys
4131                    85                   90                   95
4133 Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro
4134             100                  105                  110
4136 Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly Glu
4137         115                  120                  125
4139 His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala
4140     130                  135                  140
4143 Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe
4144 145                  150                  155                  160
4146 Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys
4147                  165                  170                  175
4149 Cys Arg Gln Gln Ser
4150                  180
4152 <210> SEQ ID NO: 40
4153 <211> LENGTH: 176
4154 <212> TYPE: PRT
4155 <213> ORGANISM: Fragaria x ananassa
4156 <223> OTHER INFORMATION: Strawberry alcohol dehydrogenase
4158 <400> SEQUENCE: 40
4159 Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
4160   1                   5                   10                  15
4162 Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
4163             20                  25                  30
4165 Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
4166             35                  40                  45
4168 Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
4169     50                  55                  60
4171 Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
4172 65                  70                  75                  80
4174 Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
4175             85                  90                  95
4177 Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
4178             100                 105                 110
4180 Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
4181         115                 120                 125
4183 Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
4184     130                 135                 140
4188 Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
4189 145                 150                 155                 160
4191 Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
4192                 165                 170                 175
4580 <210> SEQ ID NO: 50
4581 <211> LENGTH: 28
4582 <212> TYPE: DNA
4583 <213> ORGANISM: Artificial Sequence
4585 <220> FEATURE:
4586 <221> NAME/KEY:
```

The types of errors shown exist throughout the Sequence Listing. Please check subseque sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:41

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\05152002\I857518.raw**

```
4587 <222> LOCATION:
4588 <223> OTHER INFORMATION: PCR Primer
4590 <220> FEATURE:
4593 <223> OTHER INFORMATION: AAP166
4595 <400> SEQUENCE: 50
4596 cgtcgaccat tgcacgagcc acataatc        28
E--> 4599 (10) delete
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 05/15/2002
PATENT APPLICATION: US/09/857,518   TIME: 16:13:42

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\05152002\I857518.raw**

```
L:13   M:270 C: Current Application Number differs, Replaced Current Application Number
L:14   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:771  M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:6
L:1284 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1285 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:1410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1392
L:1686 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:14
L:2330 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:19
L:2427 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:20
L:2518 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:21
L:2617 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:22
L:2708 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:23
L:2799 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:24
L:2903 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:25
L:2997 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:26
L:3095 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:27
L:3180 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:28
L:3278 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:29
L:3409 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:30
L:3482 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:31
L:3554 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:32
L:3618 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:33
L:3681 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:34
L:4114 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:39
L:4158 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:40
L:4200 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:41
L:4359 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:43
L:4521 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4525 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:4526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:4540 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4545 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:47
L:4548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:4555 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:4556 M:283 W: Missing Blank Line separator, <220> field identifier
L:4562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:4570 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:4586 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50
L:4599 M:254 E: No. of Bases conflict, this line has no nucleotides.
```

VERIFICATION SUMMARY   DATE: 10/16/2003
PATENT APPLICATION: **US/09/857,518A**   TIME: 11:46:14

Input Set : **A:\CRFSEQLIST062203.txt**
Output Set: **N:\CRF4\10162003\I857518A.raw**

```
  4 M:271 C: Current Filing Date differs, Replaced Current Filing Date
361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1392
382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
```